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1. (Once Amended) An isolated polypeptide encoded by the polynucleotide of claim 3.

3. (Once Amended) An isolated polynucleotide encoding a polypeptide selected from the group consisting of:

a) a polypeptide comprising the amino acid sequence of SEQ ID NO:2,

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b) a polypeptide comprising a naturally occurring human variant of the amino acid sequence of SEQ ID NO:2,

c) a fragment of a polypeptide having the amino acid sequence of SEQ ID NO:2, wherein said fragment binds thrombin, and

d) an immunogenic fragment of a polypeptide having the amino acid sequence of SEQ ID NO:2, wherein said fragment comprises at least 13 contiguous amino acid residues of SEQ ID NO:2.

4. An isolated polynucleotide of claim 3 encoding a polypeptide comprising the amino acid sequence of SEQ ID NO:2.

5. An isolated polynucleotide of claim 4 comprising the polynucleotide sequence of SEQ ID NO:1.

6. A recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide of claim 3.

7. A cell transformed with a recombinant polynucleotide of claim 6.

9. (Once Amended) A method of producing a polypeptide encoded by a polynucleotide of claim 3, the method comprising:

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a) culturing a cell under conditions wherein the polypeptide is expressed, and wherein said cell is transformed with a recombinant polynucleotide, and said recombinant polynucleotide comprises a

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promoter sequence operably linked to a polynucleotide of claim 3, and

b) recovering the polypeptide so expressed.

10. A method of claim 9, wherein the polypeptide comprises the amino acid sequence of SEQ ID NO:2.

12. An isolated polynucleotide selected from the group consisting of:

a) a polynucleotide comprising the polynucleotide sequence of SEQ ID NO:1,

b) a polynucleotide comprising a naturally occurring human variant of the polynucleotide sequence of SEQ ID NO:1,

c) a polynucleotide complementary to a polynucleotide of a),

d) a polynucleotide complementary to a polynucleotide of b), and

e) an RNA equivalent of a)-d).

13. (Once Amended) An isolated polynucleotide comprising at least 60 contiguous nucleotides of a polynucleotide selected from the group consisting of:

a) a polynucleotide consisting of the polynucleotide sequence of SEQ ID NO:1,

B4 b) a polynucleotide consisting of a naturally occurring human variant of the polynucleotide sequence of SEQ ID NO:1,

c) a polynucleotide complementary to a polynucleotide of a),

d) a polynucleotide complementary to a polynucleotide of b), and

e) an RNA equivalent of a)-d).

14. A method of detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 12, the method comprising:

a) hybridizing the sample with a probe comprising at least 20 contiguous nucleotides comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions whereby a hybridization complex

is formed between said probe and said target polynucleotide or fragments thereof, and

b) detecting the presence or absence of said hybridization complex, and, optionally, if present, the amount thereof.

15. A method of claim 14, wherein the probe comprises at least 60 contiguous nucleotides.

16. A method of detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 12, the method comprising:

a) amplifying said target polynucleotide or fragment thereof using polymerase chain reaction amplification, and

b) detecting the presence or absence of said amplified target polynucleotide or fragment thereof, and, optionally, if present, the amount thereof.

28. A method of screening a compound for effectiveness in altering expression of a target polynucleotide, wherein said target polynucleotide comprises a sequence of claim 5, the method comprising:

a) exposing a sample comprising the target polynucleotide to a compound, under conditions suitable for the expression of the target polynucleotide,

b) detecting altered expression of the target polynucleotide, and

c) comparing the expression of the target polynucleotide in the presence of varying amounts of the compound and in the absence of the compound.

29. A method of assessing toxicity of a test compound, the method comprising:

a) treating a biological sample containing nucleic acids with the test compound,

b) hybridizing the nucleic acids of the treated biological sample with a probe comprising at least 20 contiguous nucleotides of a polynucleotide of claim 12 under conditions whereby a specific hybridization complex is formed between said probe and a target polynucleotide in the biological sample, said target polynucleotide comprising a polynucleotide sequence of a polynucleotide of claim

12 or fragment thereof,

c) quantifying the amount of hybridization complex, and

d) comparing the amount of hybridization complex in the treated biological sample with the amount of hybridization complex in an untreated biological sample, wherein a difference in the amount of hybridization complex in the treated biological sample is indicative of toxicity of the test compound.

46. A microarray wherein at least one element of the microarray is a polynucleotide of claim 13.

47. A method of generating an expression profile of a sample which contains polynucleotides, the method comprising:

a) labeling the polynucleotides of the sample,

b) contacting the elements of the microarray of claim 46 with the labeled polynucleotides of the sample under conditions suitable for the formation of a hybridization complex, and

c) quantifying the expression of the polynucleotides in the sample.

56. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:2.

57. A polynucleotide of claim 12, comprising the polynucleotide sequence of SEQ ID NO:1.

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58. (New) An isolated polynucleotide of claim 12, comprising a naturally occurring human variant of the polynucleotide sequence of SEQ ID NO:1.